

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/552,552
Source: P4710
Date Processed by STIC: 10/20/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/20/2005

PATENT APPLICATION: US/10/552,552

TIME: 09:43:22

Input Set : N:\RJAVED\10552552.txt

Output Set: N:\CRF4\10202005\J552552.raw

3 <110> APPLICANT: Bayer BioScience N.V.
 4 De Block, Marc
 6 <120> TITLE OF INVENTION: Methods and means for increasing the tolerance of plants to stress conditions.
 7
 9 <130> FILE REFERENCE: BCS 03 2002 WO1
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/552,552
 C--> 11 <141> CURRENT FILING DATE: 2005-10-07
 11 <150> PRIOR APPLICATION NUMBER: EP03076044.1
 12 <151> PRIOR FILING DATE: 2003-04-09
 14 <150> PRIOR APPLICATION NUMBER: US 60/496,688
 15 <151> PRIOR FILING DATE: 2003-08-21
 17 <160> NUMBER OF SEQ ID NOS: 25
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 548
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Arabidopsis thaliana
 26 <400> SEQUENCE: 1
 28 Met Glu Asn Arg Glu Asp Leu Asn Ser Ile Leu Pro Tyr Leu Pro Leu
 29 1 5 10 15
 32 Val Ile Arg Ser Ser Ser Leu Tyr Trp Pro Pro Arg Val Val Glu Ala
 33 20 25 30
 36 Leu Lys Ala Met Ser Glu Gly Pro Ser His Ser Gln Val Asp Ser Gly
 37 35 40 45
 40 Glu Val Leu Arg Gln Ala Ile Phe Asp Met Arg Arg Ser Leu Ser Phe
 41 50 55 60
 44 Ser Thr Leu Glu Pro Ser Ala Ser Asn Gly Tyr Ala Phe Leu Phe Asp
 45 65 70 75 80
 48 Glu Leu Ile Asp Glu Lys Glu Ser Lys Arg Trp Phe Asp Glu Ile Ile
 49 85 90 95
 52 Pro Ala Leu Ala Ser Leu Leu Leu Gln Phe Pro Ser Leu Leu Glu Val
 53 100 105 110
 56 His Phe Gln Asn Ala Asp Asn Ile Val Ser Gly Ile Lys Thr Gly Leu
 57 115 120 125
 60 Arg Leu Leu Asn Ser Gln Gln Ala Gly Ile Val Phe Leu Ser Gln Glu
 61 130 135 140
 64 Leu Ile Gly Ala Leu Leu Ala Cys Ser Phe Phe Cys Leu Phe Pro Asp
 65 145 150 155 160
 68 Asp Asn Arg Gly Ala Lys His Leu Pro Val Ile Asn Phe Asp His Leu
 69 165 170 175
 72 Phe Ala Ser Leu Tyr Ile Ser Tyr Ser Gln Ser Gln Glu Ser Lys Ile
 73 180 185 190
 76 Arg Cys Ile Met His Tyr Phe Glu Arg Phe Cys Ser Cys Val Pro Ile

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77          195          200          205
80 Gly Ile Val Ser Phe Glu Arg Lys Ile Thr Ala Ala Pro Asp Ala Asp
81      210          215          220
84 Phe Trp Ser Lys Ser Asp Val Ser Leu Cys Ala Phe Lys Val His Ser
85 225          230          235          240
88 Phe Gly Leu Ile Glu Asp Gln Pro Asp Asn Ala Leu Glu Val Asp Phe
89          245          250          255
92 Ala Asn Lys Tyr Leu Gly Gly Gly Ser Leu Ser Arg Gly Cys Val Gln
93          260          265          270
96 Glu Glu Ile Arg Phe Met Ile Asn Pro Glu Leu Ile Ala Gly Met Leu
97      275          280          285
100 Phe Leu Pro Arg Met Asp Asp Asn Glu Ala Ile Glu Ile Val Gly Ala
101      290          295          300
104 Glu Arg Phe Ser Cys Tyr Thr Gly Tyr Ala Ser Ser Phe Arg Phe Ala
105 305          310          315          320
108 Gly Glu Tyr Ile Asp Lys Lys Ala Met Asp Pro Phe Lys Arg Arg Arg
109          325          330          335
112 Thr Arg Ile Val Ala Ile Asp Ala Leu Cys Thr Pro Lys Met Arg His
113          340          345          350
116 Phe Lys Asp Ile Cys Leu Leu Arg Glu Ile Asn Lys Ala Leu Cys Gly
117      355          360          365
120 Phe Leu Asn Cys Ser Lys Ala Trp Glu His Gln Asn Ile Phe Met Asp
121      370          375          380
124 Glu Gly Asp Asn Glu Ile Gln Leu Val Arg Asn Gly Arg Asp Ser Gly
125 385          390          395          400
128 Leu Leu Arg Thr Glu Thr Thr Ala Ser His Arg Thr Pro Leu Asn Asp
129          405          410          415
132 Val Glu Met Asn Arg Glu Lys Pro Ala Asn Asn Leu Ile Arg Asp Phe
133          420          425          430
136 Tyr Val Glu Gly Val Asp Asn Glu Asp His Glu Asp Asp Gly Val Ala
137      435          440          445
140 Thr Gly Asn Trp Gly Cys Gly Val Phe Gly Gly Asp Pro Glu Leu Lys
141      450          455          460
144 Ala Thr Ile Gln Trp Leu Ala Ala Ser Gln Thr Arg Arg Pro Phe Ile
145 465          470          475          480
148 Ser Tyr Tyr Thr Phe Gly Val Glu Ala Leu Arg Asn Leu Asp Gln Val
149          485          490          495
152 Thr Lys Trp Ile Leu Ser His Lys Trp Thr Val Gly Asp Leu Trp Asn
153          500          505          510
156 Met Met Leu Glu Tyr Ser Ala Gln Arg Leu Tyr Lys Gln Thr Ser Val
157      515          520          525
160 Gly Phe Phe Ser Trp Leu Leu Pro Ser Leu Ala Thr Thr Asn Lys Ala
161      530          535          540
164 Ile Gln Pro Pro
165 545
168 <210> SEQ ID NO: 2
169 <211> LENGTH: 169
170 <212> TYPE: PRT
171 <213> ORGANISM: Solanum tuberosum

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173 <400> SEQUENCE: 2

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175 Met Glu Asn Arg Glu Asp Val Lys Ser Ile Leu Pro Phe Leu Pro Val
176 1 5 10 15
179 Cys Leu Arg Ser Ser Ser Leu Phe Trp Pro Pro Leu Val Val Glu Ala
180 20 25 30
183 Leu Lys Ala Leu Ser Glu Gly Pro His Tyr Ser Asn Val Asn Ser Gly
184 35 40 45
187 Gln Val Leu Phe Leu Ala Ile Ser Asp Ile Arg Asn Ser Leu Ser Leu
188 50 55 60
191 Pro Asp Ser Ser Ile Ser Ser Ser Ala Ser Asp Gly Phe Ser Leu Leu
192 65 70 75 80
195 Phe Asp Asp Leu Ile Pro Arg Asp Glu Ala Val Lys Trp Phe Lys Glu
196 85 90 95
199 Val Val Pro Lys Met Ala Asp Leu Leu Arg Leu Pro Ser Leu Leu
200 100 105 110
203 Glu Ala His Tyr Glu Lys Ala Asp Gly Gly Ile Val Lys Gly Val Asn
204 115 120 125
207 Thr Gly Leu Arg Leu Leu Glu Ser Gln Gln Pro Gly Ile Val Phe Leu
208 130 135 140
211 Ser Gln Glu Leu Val Gly Ala Leu Leu Ala Cys Ser Phe Phe Cys Tyr
212 145 150 155 160
215 Ser Leu Pro Met Ile Glu Val Ser Val
216 165

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219 <210> SEQ ID NO: 3

220 <211> LENGTH: 1647

221 <212> TYPE: DNA

222 <213> ORGANISM: Arabidopsis thaliana

224 <400> SEQUENCE: 3

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227 tcgtcgctgt attggccgcc gcgtgtggtg gaggcgttaa aggcaatgtc tgaaggacca 120
229 tctcacagcc aagttgactc aggagagggt ctacggcaag ctattttcga tatgagacga 180
231 tccttatctt tctctactct cgagccatct gcttctaatt gctacgcatt tctctttgac 240
233 gaattgattg atgagaaaga atcaaagaga tggttcgatg agattatccc agcattggcg 300
235 agcttacttc tacagtttcc atctctgtta gaagtgcatt tccaaaatgc tgataatatt 360
237 gttagtggaa tcaaaaccgg tcttcgtttg ttaaattccc aacaagctgg cattgttttc 420
239 ctacagccagg agttgattgg agctcttctt gcatgctctt tcttttgttt gtttccggat 480
241 gataatagag gtgcaaaaaca ccttccagtc atcaactttg atcatttggt tgcaagcctt 540
243 tatataagtt atagtcaaag tcaagaaaagc aagataagat gtattatgca ttactttgaa 600
245 aggttttgct cctgcgtgcc tattggtatt gtttcatttg aacgcaagat taccgctgct 660
247 cctgatgctg atttctggag caagtctgac gtttctcttt gtgcatttaa ggttcactct 720
249 tttgggttaa ttgaagatca acctgacaat gctctcgaag tggactttgc aaacaagtat 780
251 ctcggaagggtg gttccctaag tagaggggtgc gtgcaggaag agatacgctt catgattaac 840
253 cctgaattaa tcgctggcat gcttttcttg cctcggatgg atgacaatga agctatagaa 900
255 atagttggtg cggaaagatt ttcattgttac acaggggtatg catcttcggt tcgggttgct 960
257 ggtgagtaca ttgacaaaaa ggcaatggat cctttcaaaa ggccaagaac cagaattggt 1020
259 gcaattgatg cattatgtac accgaagatg agacacttta aagatatatg tcttttaagg 1080
261 gaaattaata aggcaactatg tggtttttta aattgtagca aggcttggga gcaccagaat 1140
263 atattcatgg atgaaggaga taatgaaatt cagcttgccc gaaacggcag agattctggt 1200
265 cttctgcgta cagaaactac tgcgtcacac cgaactccac taaatgatgt tgagatgaat 1260

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267 agagaaaagc ctgctaacaa tcttatcaga gatttttatg tggaaggagt tgataacgag 1320
269 gatcatgaag atgatggtgt cgcgacaggg aattggggat gtggtgtttt tggaggagac 1380
271 ccagagctaa aggctacgat acaatggctt gctgcttccc agactcgaag accatttata 1440
273 tcatattaca cctttggagt agaggcactc cgaaacctag atcaggtgac gaagtggatt 1500
275 ctttcccata aatggactgt tggagatctg tggaaacatga tgttagaata ttctgctcaa 1560
277 aggetctaca agcaaaccag tgttggtctt ttttcttggc tacttccatc tctagctacc 1620
279 accaacaaaag ctatccagcc gccttga 1647
282 <210> SEQ ID NO: 4
283 <211> LENGTH: 598
284 <212> TYPE: DNA
285 <213> ORGANISM: Solanum tuberosum
287 <400> SEQUENCE: 4
288 gcaatggaga atagagaaga cgtgaagtca atccttccct ttttgccggt gtgtctccga 60
290 tcatcttctc ttttctggcc gccgctagtt gttgaagcac tgaaagccct ctctgaaggc 120
292 cctcattaca gcaatgttaa ctccggccaa gtccctcttc tcgcaatctc cgacattcgg 180
294 aattcccttt cactacctga ttcttcaatt tcctcttctg cttcagacgg attttctctc 240
296 ttatttgatg atttaattcc tagggatgaa gctgttaaag ggttcaaaga agtgggtgccg 300
298 aaaatggcgg atttgctatt gcggttgccct tccttattgg aggtcacta tgagaaggct 360
300 gatggtggaa ttgttaaagg agtcaacact ggtcttcgct tattggaatc acaacagcct 420
302 ggcattgttt tcctcagtcg ggaattagtc ggtgctcttc ttgcatgttc cttcttttgc 480
304 tattccctac caatgataga ggtatctgta tgatcagtat gacgagaaat ttgaaaataa 540
306 attgaagtgc attcttcact attttgagag gattggctca ttgatacctg cgggctac 598
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310 <211> LENGTH: 37
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: oligonucleotide primer ParGAt1
317 <400> SEQUENCE: 5
318 ggatcccctg caggacaaaa aggcaatgga tcctttc 37
321 <210> SEQ ID NO: 6
322 <211> LENGTH: 39
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: oligonucleotide primer ParGAt2
329 <400> SEQUENCE: 6
330 gcacgaattc gcggccgcgg tgctcccaag ccttgctac 39
333 <210> SEQ ID NO: 7
334 <211> LENGTH: 39
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: oligonucleotide primer ParGSt1
341 <400> SEQUENCE: 7
342 ggatcccctg caggctcact atgagaaggc tgatggtgg 39
345 <210> SEQ ID NO: 8
346 <211> LENGTH: 43
347 <212> TYPE: DNA

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348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: oligonucleotide primer ParGSt2
353 <400> SEQUENCE: 8
354 gcacgaattc gcggccgcgt catactgatc atacagatac etc 43
357 <210> SEQ ID NO: 9
358 <211> LENGTH: 13466
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: nucleotide sequence of pTVE428
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (198)..(222)
368 <223> OTHER INFORMATION: Right T-DNA border
371 <220> FEATURE:
372 <221> NAME/KEY: misc_feature
373 <222> LOCATION: (983)..(273)
374 <223> OTHER INFORMATION: 3' ocs (3' untranslated end of octopine synthase gene)
377 <220> FEATURE:
378 <221> NAME/KEY: misc_feature
379 <222> LOCATION: (995)..(1155)
380 <223> OTHER INFORMATION: part of poly (ADP-ribose) glycohydrolase
383 <220> FEATURE:
384 <221> NAME/KEY: misc_feature
385 <222> LOCATION: (1929)..(1188)
386 <223> OTHER INFORMATION: intron 2 from the Pdk gene of Flaveria
389 <220> FEATURE:
390 <221> NAME/KEY: misc_feature
391 <222> LOCATION: (2122)..(1962)
392 <223> OTHER INFORMATION: part of poly (ADP-ribose) glycohydrolase
395 <220> FEATURE:
396 <221> NAME/KEY: misc_feature
397 <222> LOCATION: (3476)..(2131)
398 <223> OTHER INFORMATION: 35S promoter region from Cauliflower Mosaic Virus
401 <220> FEATURE:
402 <221> NAME/KEY: misc_feature
403 <222> LOCATION: (3948)..(3737)
404 <223> OTHER INFORMATION: 3' untranslated end of gene 7 from Agrobacterium tumefaciens
407 <220> FEATURE:
408 <221> NAME/KEY: misc_feature
409 <222> LOCATION: (4521)..(3970)
410 <223> OTHER INFORMATION: bar coding region
413 <220> FEATURE:
414 <221> NAME/KEY: misc_feature
415 <222> LOCATION: (6247)..(4522)
416 <223> OTHER INFORMATION: PSSuAra promoter region
419 <220> FEATURE:
420 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 2,8,9,10,14,15,16,17,19,27,28,29
Seq#:11; Xaa Pos. 3,10,13,14,17,18,19
Seq#:12; Xaa Pos. 2,3,4,6,7,8,9
Seq#:13; Xaa Pos. 3,4,7,8
Seq#:14; Xaa Pos. 2,3,4,5,7
Seq#:21; N Pos. 18

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10552552.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
M:341 Repeated in SeqNo=10
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:1041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1056 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1053
L:1384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0